

>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
HSA303077 Homo sapiens mRNA for mitochondrial RNA
splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
variant
Length = 1448

Score = 760 bits (1940), Expect = 0.0
Identities = 364/364 (100%), Positives = 364/364 (100%)
Frame = +3

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Show:

☐ 1: AJ303077. Homo sapiens mRNA...[gi:12666719] Links

LOCUS HSA303077 1448 bp mRNA linear PRI 26-APR-2001
DEFINITION Homo sapiens mRNA for mitochondrial RNA splicing protein 3/4
(HMRS3/4 gene), 1448 bp cDNA splice variant.

ACCESSION AJ303077

VERSION AJ303077.1 GI:12666719

KEYWORDS HMRS3/4 gene; mitochondrial RNA splicing protein 3/4.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Li, F.Y., Nikali, K., Gregan, J., Leibiger, I., Leibiger, B.,
Schweyen, R., Larsson, C. and Suomalainen, A.

TITLE Characterization of a novel human putative mitochondrial
transporter homologous to the yeast mitochondrial RNA splicing
proteins 3 and 4

JOURNAL FEBS Lett. 494 (1-2), 79-84 (2001)

MEDLINE 21195335

PUBMED 11297739

REFERENCE 2 (bases 1 to 1448)

AUTHORS Nikali, K.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2000) Nikali K., Human Molecular Genetics,
National Public Health Institute, Mannerheimintie 166, Helsinki,
FI-00300, FINLAND

FEATURES

Location/Qualifiers

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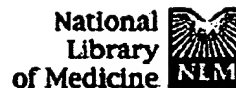
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☐ 1: FEBS Lett. 2001 Apr 6;494(1-2):79-84.

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ELSEVIER
FULL-TEXT ARTICLE

Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing proteins 3 and 4.

Li FY, Nikali K, Gregan J, Leibiger I, Leibiger B, Schweyen R, Larsson C, Suomalainen A.

Department of Molecular Medicine, CMM, Karolinska Hospital, Stockholm, Sweden. fangyuan.li@cmm.ki.se

We report here a novel human gene, hMRS3/4, encoding a putative mitochondrial transporter structurally and functionally homologous to the yeast mitochondrial RNA splicing proteins 3 and 4. These proteins belong to the family of mitochondrial carrier proteins (MCF) and are likely to function as solute carriers. hMRS3/4 spans approximately 10 kb of genomic DNA on chromosome 10q24 and consists of four exons that encode a 364-aa protein with six transmembrane domains. A putative splice variant, encoding a 177-aa protein with three transmembrane domains, was also identified. hMRS3/4 has a well-conserved signature sequence of MCF and is targeted into the mitochondria. When expressed in yeast, hMRS3/4 efficiently restores the mitochondrial functions in mrs3(o)mrs4(o) knock-out mutants. Ubiquitous expression in human tissues and a well-conserved structure and function suggest an important role for hMRS3/4 in human cells.

MeSH Terms:

- Alternative Splicing*
- Amino Acid Sequence
- Base Sequence
- Carrier Proteins/genetics*
- Carrier Proteins/metabolism
- Chromosome Mapping
- Chromosomes, Human, Pair 10*
- DNA, Complementary
- Fungal Proteins/genetics
- Gene Expression Profiling
- Human
- Membrane Transport Proteins*

- Mitochondria/metabolism*
- Molecular Sequence Data
- Mutagenesis
- Ophthalmoplegia, Chronic Progressive External/genetics
- RNA Splicing
- Repressor Proteins*
- Saccharomyces cerevisiae/genetics
- Saccharomyces cerevisiae Proteins*
- Spinocerebellar Ataxias/genetics
- Support, Non-U.S. Gov't
- Tissue Distribution
- Transfection

Substances:

- Carrier Proteins
- DNA, Complementary
- Fungal Proteins
- Membrane Transport Proteins
- Repressor Proteins
- SLC25A28 protein, human
- Saccharomyces cerevisiae Proteins
- MRS4 protein, S cerevisiae
- MRS3 protein, S cerevisiae

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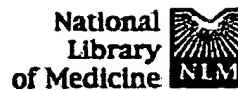
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- GENBANK/AJ303078

PMID: 11297739 [PubMed - indexed for MEDLINE]

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1: J Mol Biol. 1991 Jan 5;217(1):23-37.

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MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family.

Wiesenberger G, Link TA, von Ahsen U, Waldherr M, Schweyen RJ.

Institut für Mikrobiologie und Genetik Universität Wien, Austria.

When present in high copy number plasmids, the nuclear genes MRS3 and MRS4 from *Saccharomyces cerevisiae* can suppress the mitochondrial RNA splicing defects of several mit- intron mutations. Both genes code for closely related proteins of about Mr 32,000; they are 73% identical. Sequence comparisons indicate that MRS3 and MRS4 may be related to the family of mitochondrial carrier proteins. Support for this notion comes from a structural analysis of these proteins. Like the ADP/ATP carrier protein (AAC), the mitochondrial phosphate carrier protein (PiC) and the uncoupling protein (UCP), the two MRS proteins have a tripartite structure; each of the three repeats consists of two hydrophobic domains that are flanked by specific amino acid residues. The spacing of these specific residues is identical in all domains of all proteins of the family, whereas spacing between the hydrophobic domains is variable. Like the AAC protein, the MRS3 and MRS4 proteins are imported into mitochondria in vitro and without proteolytic cleavage of a presequence and they are located in the inner mitochondrial membrane. In vivo studies support this mitochondrial localization of the MRS proteins. Overexpression of the MRS3 and MRS4 proteins causes a temperature-dependent petite phenotype; this is consistent with a mitochondrial function of these proteins. Disruption of these genes affected neither mitochondrial functions nor cellular viability. Their products thus have no essential function for mitochondrial biogenesis or for whole yeast cells that could not be taken over by other gene products. The findings are discussed in relation to possible functions of the MRS proteins in mitochondrial solute translocation and RNA splicing.

PMID: 1703236 [PubMed - indexed for MEDLINE]

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Score = 760 bits (1940), Expect = 0.0
Identities = 364/364 (100%), Positives = 364/364 (100%)
Frame = +2

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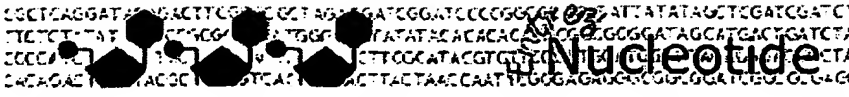
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☐ 1: BC047312. Homo sapiens solu...[gi:28703799] Links

LOCUS BC047312 1550 bp mRNA linear PRI 11-DEC-2003
 DEFINITION Homo sapiens solute carrier family 25, member 28, mRNA (cDNA clone IMAGE:5199184), partial cds.

ACCESSION BC047312
 VERSION BC047312.1 GI:28703799

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1550)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 1550)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (28-FEB-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).

Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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//

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Jan 29 2004 15:38:25

>BC058937 ACCESSION:BC058937 NID: gi 37747474 gb BC058937.1 Homo
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clone MGC:65184 IMAGE:6139015), complete cds
Length = 1472

Score = 760 bits (1940), Expect = 0.0
Identities = 364/364 (100%), Positives = 364/364 (100%)
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Query: 121 IIRTEGLWRPMPRLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
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Query: 361 RAGK 364
RAGK
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 Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for

Limits Preview/Index History Clipboard Details

Show:

☐ 1: BC058937. Homo sapiens solu...[gi:37747474] Links

LOCUS BC058937 1472 bp mRNA linear PRI 11-DEC-2003
 DEFINITION Homo sapiens solute carrier family 25, member 28, mRNA (cDNA clone MGC:65184 IMAGE:6139015), complete cds.

ACCESSION BC058937
 VERSION BC058937.1 GI:37747474
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1472)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932

REFERENCE 2 (bases 1 to 1472)

AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letricia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 119 Row: k Column: 24.

FEATURES

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1441 taaaaagcct ttaaattaaa aaaaaaaaaa aa

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Jan 29 2004 15:38:25

characterize the protein. A starting material that can only be used to produce a final product does not have a substantial asserted utility in those instances where the final product is not supported by a specific and substantial utility. In this case none of the proteins that are to be produced as final products resulting from processes involving the claimed cDNA have asserted or identified specific and substantial utilities. The research contemplated by Applicants to characterize potential protein products, especially their biological activities, does not constitute a specific and substantial utility. Identifying and studying the properties of the protein itself or the mechanisms in which the protein is involved does not define a "real world" context of use. Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed. Neither the specification as filed nor any art of record discloses or suggests any property or activity for the cDNA compounds such that another non-asserted utility would be well established for the compounds.

Claim 1 is also rejected under 35 U.S.C. § 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art would not know how to use the claimed invention.

Example 10: DNA Fragment encoding a Full Open Reading Frame (ORF)

Specification: The specification discloses that a cDNA library was prepared from human kidney epithelial cells and 5000 members of this library were

sequenced and open reading frames were identified. The specification discloses a Table that indicates that one member of the library having SEQ ID NO: 2 has a high level of homology to a DNA ligase. The specification teaches that this complete ORF (SEQ ID NO: 2) encodes SEQ ID NO: 3. An alignment of SEQ ID NO: 3 with known amino acid sequences of DNA ligases indicates that there is a high level of sequence conservation between the various known ligases. The overall level of sequence similarity between SEQ ID NO: 3 and the consensus sequence of the known DNA ligases that are presented in the specification reveals a similarity score of 95%. A search of the prior art confirms that SEQ ID NO: 2 has high homology to DNA Ligase encoding nucleic acids and that the next highest level of homology is to alpha-actin. However, the latter homology is only 50%. Based on the sequence homologies, the specification asserts that SEQ ID NO: 2 encodes a DNA ligase.

Claim 1: An isolated and purified nucleic acid comprising SEQ ID NO: 2.

Analysis: The following analysis includes the questions that need to be asked according to the guidelines and the answers to those questions based on the above facts:

1) Based on the record, is there a "well established utility" for the claimed invention? Based upon applicant's disclosure and the results of the PTO search, there is no reason to doubt the assertion that SEQ ID NO: 2 encodes a DNA ligase. Further, DNA ligases have a well-established use in the molecular biology art based on this class of protein's ability to ligate DNA. Consequently the answer to the question is yes.

Note that if there is a well-established utility already associated with the claimed invention, the utility need not be asserted in the specification as filed. In order to determine whether the claimed invention has a well-established utility the examiner must determine that the invention has a specific, substantial and credible utility that would have been readily apparent to one of skill in the art. In this case SEQ ID NO: 2 was shown to encode a DNA ligase that the artisan would have recognized as having a specific, substantial and credible utility based on its enzymatic activity.

Thus, the conclusion reached from this analysis is that a 35 U.S.C. § 101 rejection and a 35 U.S.C. § 112, first paragraph, utility rejection should not be made.

Example 11: Animals with Uncharacterized Human Genes

Specification: Kidney cells from a patient with Polycystic Kidney (PCK) Disease have been used to make a cDNA library. From this library 8000 nucleotide "fragments" have been sequenced but not yet used to express proteins in a transformed host cell nor have they been characterized in any other way. The 50 longest fragments, SEQ ID NO: 1-50, respectively, have been used to make transgenic mice. None of the 50 lines of mice have developed Polycystic Kidney Disease to date. The asserted utility is the use of the mice to research human genes from diseased human kidneys. The disease is inheritable, but chromosomal loci have not yet been identified. Neither the absence or presence of a specific protein has been identified with the disease condition.

>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
HSA303077 Homo sapiens mRNA for mitochondrial RNA
splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
variant
Length = 1448

Score = 405 bits (1030), Expect = e-111
Identities = 192/192 (100%), Positives = 192/192 (100%)
Frame = +3

Query: 1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG
Sbjct: 30 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 209

Query: 61 PDYEALPAGATVTTHMVAGAVAGILEHCVMPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
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Sbjct: 210 PDYEALPAGATVTTHMVAGAVAGILEHCVMPIDCVKTRMQSLQPDPAARYRNVLEALWR 389

Query: 121 IIRTEGLWRPMPRLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
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TLLHDAAMNP AE
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>BC058937 ACCESSION:BC058937 NID: gi 37747474 gb BC058937.1 Homo
sapiens solute carrier family 25, member 28, mRNA (cDNA
clone MGC:65184 IMAGE:6139015), complete cds
Length = 1472

Score = 405 bits (1030), Expect = e-111
Identities = 192/192 (100%), Positives = 192/192 (100%)
Frame = +3

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TLLHDAAMNPAAE
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>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
HSA303077 Homo sapiens mRNA for mitochondrial RNA
splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
variant
Length = 1448

Score = 405 bits (1030), Expect = e-111
Identities = 192/192 (100%), Positives = 192/192 (100%)
Frame = +3

Query: 1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
MELEGRGAGGVAGGPAAGPGRSPGESALLDGLQRGVGRGAGGGEAGACRPPVRQDPDSG
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Query: 121 IIRTEGLWRPMPRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
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Sbjct: 390 IIRTEGLWRPMPRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 569

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Sbjct: 570 TLLHDAAMNPAE 605

>BC047312 ACCESSION:BC047312 NID: gi 28703799 gb BC047312.1 Homo
sapiens solute carrier family 25, member 28, mRNA (cDNA
clone IMAGE:5199184), partial cds
Length = 1550

Score = 405 bits (1030), Expect = e-111
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Frame = +2

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IIRTEGLWRPMPRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA
Sbjct: 437 IIRTEGLWRPMPRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 616

Query: 181 TLLHDAAMNPAE 192
TLLHDAAMNPAE
Sbjct: 617 TLLHDAAMNPAE 652

>BC058937 ACCESSION:BC058937 NID: gi 37747474 gb BC058937.1 Homo
sapiens solute carrier family 25, member 28, mRNA (cDNA
clone MGC:65184 IMAGE:6139015), complete cds
Length = 1472

Score = 405 bits (1030), Expect = e-111
Identities = 192/192 (100%), Positives = 192/192 (100%)
Frame = +3

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Query: 181 TLLHDAAMNP AE 192
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Sbjct: 579 TLLHDAAMNP AE 614
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>AJ303077 ACCESSION:AJ303077 NID: gi 12666719 emb AJ303077.1
HSA303077 Homo sapiens mRNA for mitochondrial RNA
splicing protein 3/4 (HMRS3/4 gene), 1448 bp cDNA splice
variant
Length = 1448

Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
Frame = +3

Query: 1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 60
MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 327 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 506

Query: 61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 507 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 605

>BC047312 ACCESSION:BC047312 NID: gi 28703799 gb BC047312.1 Homo
sapiens solute carrier family 25, member 28, mRNA (cDNA
clone IMAGE:5199184), partial cds
Length = 1550

Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
Frame = +2

Query: 1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 60
MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 374 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 553

Query: 61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 554 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 652

>BC058937 ACCESSION:BC058937 NID: gi 37747474 gb BC058937.1 Homo
sapiens solute carrier family 25, member 28, mRNA (cDNA
clone MGC:65184 IMAGE:6139015), complete cds
Length = 1472

Identities = 93/93 (100%), Positives = 93/93 (100%), Gaps = 0/93 (0%)
Frame = +3

Query: 1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 60
MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL
Sbjct: 336 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPGRGLNVTATGAGPAHALYFACYEKLKKTL 515

Query: 61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
Sbjct: 516 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 614

Query= SEQ ID NO:1
 (1095 letters)

Sequences producing significant alignments:

AL353719.10.1.123160

Score E
 (bits) Value
1031 0.0

>AL353719.10.1.123160
 Length = 123160

Identities = 520/520 (100%)
 Strand = Plus / Minus

Query: 576 agtgggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 635
 |||
 Sbjct: 82990 agtgggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 82931

Query: 636 acgggcagtggtggcaaaatgaaggggccggggcctttaccgcagctacaccaccagct 695
 |||
 Sbjct: 82930 acgggcagtggtggcaaaatgaaggggccggggcctttaccgcagctacaccaccagct 82871

Query: 696 gaccatgaacgttcctttccaagccattcattcatgacctatgaattcctgcaggagca 755
 |||
 Sbjct: 82870 gaccatgaacgttcctttccaagccattcattcatgacctatgaattcctgcaggagca 82811

Query: 756 ctttaacccccagagacgggtacaaccaagctcccacgtcctctctggagcttgcgagg 815
 |||
 Sbjct: 82810 ctttaacccccagagacgggtacaaccaagctcccacgtcctctctggagcttgcgagg 82751

Query: 816 agctgtagctgccgcagccacaacccccactggacgtttgcaaaacactgctcaacacca 875
 |||
 Sbjct: 82750 agctgtagctgccgcagccacaacccccactggacgtttgcaaaacactgctcaacacca 82691

Query: 876 ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt 935
 |||
 Sbjct: 82690 ggagtccttggctttgaactcacacattacaggacatatcacaggcatggctagtgcctt 82631

Query: 936 caggacggtatatcaagtaggtggggtagccgcctatttccgaggggtgcaggccagagt 995
 |||
 Sbjct: 82630 caggacggtatatcaagtaggtggggtagccgcctatttccgaggggtgcaggccagagt 82571

Query: 996 aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaatacct 1055
 |||
 Sbjct: 82570 aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaatacct 82511

Query: 1056 aatcactaaaaggcaagaagagtggagggtggcaagtga 1095
|||||
Sbjct: 82510 aatcactaaaaggcaagaagagtggagggtggcaagtga 82471

Identities = 291/291 (100%)
Strand = Plus / Minus

Query: 1 atggagttggagggcggggtgctggcgggtgtggcggggggcccggcggcagggcccggg 60
|||||
Sbjct: 91957 atggagttggagggcggggtgctggcgggtgtggcggggggcccggcggcagggcccggg 91898

Query: 61 cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgctgggcccgggg 120
|||||
Sbjct: 91897 cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgctgggcccgggg 91838

Query: 121 gccggcgggcggggagggccggggcctgcaggcccccggtacgacaagatccggactccggc 180
|||||
Sbjct: 91837 gccggcgggcggggagggccggggcctgcaggcccccggtacgacaagatccggactccggc 91778

Query: 181 ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 240
|||||
Sbjct: 91777 ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 91718

Query: 241 gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 291
|||||
Sbjct: 91717 gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 91667

Identities = 233/233 (100%)
Strand = Plus / Minus

Query: 290 agaccggatgcagagtctacagcctgaccagctgcccgtatcgcaatgtgttgagg 349
|||||
Sbjct: 85548 agaccggatgcagagtctacagcctgaccagctgcccgtatcgcaatgtgttgagg 85489

Query: 350 ccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacgtca 409
|||||
Sbjct: 85488 ccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacgtca 85429

Query: 410 cagcaacaggcgaggcgctgccacgccctttatTTTgcctgctacgaaaagttaaaaa 469
|||||
Sbjct: 85428 cagcaacaggcgaggcgctgccacgccctttatTTTgcctgctacgaaaagttaaaaa 85369

Query: 470 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
|||||
Sbjct: 85368 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316

Identities = 58/58 (100%)
Strand = Plus / Minus

Query: 520 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaag 577
|||||
Sbjct: 84222 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaag 84165

Query= SEQ ID NO:3
(582 letters)

Sequences producing significant alignments:

| | Score (bits) | E Value |
|--|-----------------|------------|
|--|-----------------|------------|

AL353719.10.1.123160

577 e-162

>AL353719.10.1.123160

Length = 123160

Score = 577 bits (291), Expect = e-162

Identities = 291/291 (100%)

Strand = Plus / Minus

Query: 1 atggagttggagggcggggtgctggcggtgtggcggggggcccggcggcagggcccggg 60
|||||
Sbjct: 91957 atggagttggagggcggggtgctggcggtgtggcggggggcccggcggcagggcccggg 91898

Query: 61 cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgctgggcccggggg 120
|||||
Sbjct: 91897 cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgctgggcccggggg 91838

Query: 121 gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 180
|||||
Sbjct: 91837 gccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccggc 91778

Query: 181 ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 240
|||||
Sbjct: 91777 ccggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgcc 91718

Query: 241 gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 291
|||||
Sbjct: 91717 gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag 91667

Score = 462 bits (233), Expect = e-127

Identities = 233/233 (100%)

Strand = Plus / Minus

Query: 290 agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttgagg 349
|||||
Sbjct: 85548 agacccggatgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttgagg 85489

Query: 350 ccctctggaggattataaagaacggagggcctatggaggcccatgagggggctgaacgtca 409
|||||
Sbjct: 85488 ccctctggaggattataaagaacggagggcctatggaggcccatgagggggctgaacgtca 85429

Query: 410 cagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaa 469
|||||
Sbjct: 85428 cagcaacaggcgcagggcctgcccacgccctttattttgcctgctacgaaaagttaaaaa 85369

Query: 470 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
|||||
Sbjct: 85368 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316

Score = 117 bits (59), Expect = 8e-24
Identities = 59/59 (100%)
Strand = Plus / Minus

Query: 520 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaagg 578
|||||
Sbjct: 84222 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaagg 84164

Query= SEQ ID NO:5
(693 letters)

| Sequences producing significant alignments: | Score (bits) | E Value |
|---|-----------------|------------|
|---|-----------------|------------|

| | | |
|----------------------|------------|-------|
| AL353719.10.1.123160 | <u>577</u> | e-162 |
|----------------------|------------|-------|

>AL353719.10.1.123160
Length = 123160

Score = 577 bits (291), Expect = e-162
Identities = 291/291 (100%)
Strand = Plus / Minus

| | | |
|--------------|--|-------|
| Query: 1 | atggagttggagggcggggtgctggcggtgtggcggggggcccggcggcagggccccggg | 60 |
| | | |
| Sbjct: 91957 | atggagttggagggcggggtgctggcggtgtggcggggggcccggcggcagggccccggg | 91898 |

| | | |
|--------------|--|-------|
| Query: 61 | cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggggg | 120 |
| | | |
| Sbjct: 91897 | cggagccccggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggggg | 91838 |

| | | |
|--------------|--|-------|
| Query: 121 | gccggcgggcggggagggccggggcctgcaggcccccggtacgacaagatccggactccggc | 180 |
| | | |
| Sbjct: 91837 | gccggcgggcggggagggccggggcctgcaggcccccggtacgacaagatccggactccggc | 91778 |

| | | |
|--------------|--|-------|
| Query: 181 | ccggactacgagggcgctgccggctggagccactgtcaccacgcacatggtggcagggcgcc | 240 |
| | | |
| Sbjct: 91777 | ccggactacgagggcgctgccggctggagccactgtcaccacgcacatggtggcagggcgcc | 91718 |

| | | |
|--------------|---|-------|
| Query: 241 | gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag | 291 |
| | | |
| Sbjct: 91717 | gtggcagggatcctggagcactgcgtgatgtaccccatcgactgcgtcaag | 91667 |

Score = 462 bits (233), Expect = e-127
Identities = 233/233 (100%)
Strand = Plus / Minus

| | | |
|--------------|---|-------|
| Query: 290 | agaccgggatgcagagtctacagcctgacctgacctgcccgtatcgcaatgtgttgagg | 349 |
| | | |
| Sbjct: 85548 | agaccgggatgcagagtctacagcctgacctgacctgcccgtatcgcaatgtgttgagg | 85489 |

| | | |
|--------------|--|-------|
| Query: 350 | ccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacgtca | 409 |
| | | |
| Sbjct: 85488 | ccctctggaggattataagaacggagggcctatggaggcccatgagggggctgaacgtca | 85429 |

Query: 410 cagcaacaggcgagggcctgcccacgccctttattttgctgctacgaaaagttaaaaa 469
|||||
Sbjct: 85428 cagcaacaggcgagggcctgcccacgccctttattttgctgctacgaaaagttaaaaa 85369

Query: 470 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 522
|||||
Sbjct: 85368 agacattgagtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316

Score = 345 bits (174), Expect = 2e-92
Identities = 174/174 (100%)
Strand = Plus / Minus

Query: 520 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 579
|||||
Sbjct: 84222 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 84163

Query: 580 aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 639
|||||
Sbjct: 84162 aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 84103

Query: 640 gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 693
|||||
Sbjct: 84102 gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 84049

Query= SEQ ID NO:11
(396 letters)

| Sequences producing significant alignments: | Score (bits) | E Value |
|---|-----------------|------------|
|---|-----------------|------------|

| | | |
|----------------------|-----|-------|
| AL353719.10.1.123160 | 446 | e-123 |
|----------------------|-----|-------|

>AL353719.10.1.123160
Length = 123160

Score = 446 bits (225), Expect = e-123
Identities = 225/225 (100%)
Strand = Plus / Minus

Query: 1 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttgaggccctctgg 60
|||||
Sbjct: 85540 atgcagagtctacagcctgacccagctgcccgctatcgcaatgtgttgaggccctctgg 85481

Query: 61 aggattataagaacggaggggcctatggaggcccatgagggggctgaacgtcacagcaaca 120
|||||
Sbjct: 85480 aggattataagaacggaggggcctatggaggcccatgagggggctgaacgtcacagcaaca 85421

Query: 121 ggcgagggcctgcccacgccctttatttgcctgctacgaaaagttaaaaaagacattg 180
|||||
Sbjct: 85420 ggcgagggcctgcccacgccctttatttgcctgctacgaaaagttaaaaaagacattg 85361

Query: 181 agtgatgtaatccaccctgggggcaatagccatattgccaatggt 225
|||||
Sbjct: 85360 agtgatgtaatccaccctgggggcaatagccatattgccaatggt 85316

Score = 345 bits (174), Expect = 1e-92
Identities = 174/174 (100%)
Strand = Plus / Minus

Query: 223 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 282
|||||
Sbjct: 84222 ggtgcggccgggtgtgtggcaacattacttcatgatgcagccatgaaccctgcggaaggt 84163

Query: 283 aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 342
|||||
Sbjct: 84162 aatgattcctcaacctatcactctgtgggcagctgcacctgtatttctttacagtttgca 84103

Query: 343 gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 396
|||||
Sbjct: 84102 gaagaaagcacatcagttttggtgggaaattctgttaccttgttttaccactag 84049



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

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Details

Display

Show:

Send to

Get Subsequence

Features

☐ 1: AL353719. Human DNA sequenc...[gi:15787725]

Links

LOCUS AL353719 123160 bp DNA linear PRI 25-SEP-2001
 DEFINITION Human DNA sequence from clone RP11-85A1 on chromosome 10, complete sequence.

ACCESSION AL353719 AC007643
 VERSION AL353719.10 GI:15787725
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 123160)

AUTHORS Ramsay, H.

TITLE Direct Submission

JOURNAL Submitted (25-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 requests: clonerequest@sanger.ac.uk

COMMENT On Sep 26, 2001 this sequence version replaced gi:14280413.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em:, EMBL; Sw:,
 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>

RP11-85A1 is from the library RPCI-11.1 constructed by the group of
 Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-85A1 It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.

The true left end of clone RP11-85A1 is at 1 in this sequence. The
 true left end of clone RP11-483F11 is at 123061 in this sequence.